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OM nucleic - nucleic search, using sw model
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REFERENCE TITLE TITLE AUTHORS MEDLINE JOURNAL PUBMED angusta

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CNS077ZN CNS075SU CNS07387

CNS078CQ 1056 bp DNA lineac 3SS 08-JUL-20 T3 end of clone BB0AA019F09 of library BB0AA from strain CBS 4732 PICATE ATTACAN TO THE PROPERTY OF Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Be-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, S., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Malpertuy, A., Malpertuy, A., Malpertuy, A., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Malpertuy, A., Neuveglise, C., Wesolowski-Louvel, M., Malpertuy, A., Neuveglise, C., Wesolowski-Louvel, M., Malpertuy, A., Neuveglise, C., Wesolowski-Louvel, M., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Malpertuy, A., Malpertuy, A., Malpertuy, A., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier-Kalogeropoulos, O., Potier-Kalogerop Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of Genomic exploration of the evolution studies yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000) Saccharomycetales; Saccharomycetaceae; Pichia. Pichia angusta Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; AL433824.1 GI:12217238 Pichia angusta. Genomic exploration of the hemiascomycetous yeasts: 13. Pichia Blandin, G., Llorente, B., Malpertuy, A., Wincker, P., Artiguenave, F. and Dujon, B. (bases 1 to 1056) (bases 1 to 1056) GSS 08-JUL-2001

AUTHORS

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                                            893 GCCGGGTGCGTTCATGACGGCGTACAATGGCATCAATGGCGTGTCGTGCAGCGAGAACCC 952
                                                                                          624 GCAGCGTGCCTTGCGAGAGATATACCTCCGTCCGTTTGAGATCGCGATCAAGGAATCCCA 565
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                                                                                                                                        833 GGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATTGCTGTGCGAGACTCCCA 892
                                                                                                                                                                                       684 GAAGCACTTIGTCGGCAACGACCAGGAGCACGAGCGTTTCAGTTCGAATTCAGTGATCTC
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                                                                                                                                                                                                                                                                                 744 GGGAATCCTGTCTGCGGCGTACATTAAGGGGTYTCAAAAGTCAGGTCTTGCTGCCACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exiguus, Saccharomyces servazzii, zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage; 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segrefégenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope.
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/note="similar to P07337 [ Beta-glucosidase precursor BGLS
] [ Kluyveromyces marxianus ] "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1313 GCCCTTGAGCAAGAAGAAGAAGACGCTGATTGTCGGCCCCAACGCCAAGCAGGCCACATA 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1193 CTCCGGAGTGACGGAGAACGGCCCCGAGACGACTGTCAACAACACCCCCCGAAACGGCAGC 1252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 GTTTTTGAGGAAAATAGCTGGTGAGGCTGTCGTGCTTCTCAAAAACAAGGATGGTGTGCT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 TGCGGGAATTGAGGACAATAAGGCAGAGGAG---CAGCGTGATACCCCCTGAAACAAGAGC 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 CAGCAAGGAGATAGGCCCG 11
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                                                                                                                                          High quality sequence stop: 280
                                                                                                                                                                   Class: BAC ends
                                                                                                                                                                                   Seq primer:
                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rdean@clemson.edu
                                                                                                                                                                                                                                                        100 Jordan Hall, Clemson Universiy, Clemson,
                                                                                                                                                                                                                                                                                                                          Contact: Dean RA
                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
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Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M., Wing,R.A. and Dean,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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                                                                /organism="Magnaporthe grisea"
/strain="70-15"
/clone_lib="CUGI Rice Blast BAC Library"
                        /clone="mgxb0010D05f"
                                           /db_xref="taxon:148305"
                                                                                                                       Location/Qualifiers
                                                                                                                                                                                   TAATACGACTCACTATAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 TCAGACGGCCCCAACGGCGTCCGTGGAACCCGCTTCTTCAACGGCGTCAGGGCGGCCTGC 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 CTGGCCGGACTCGGCGCCGCCATCGTGCGCGCATTCAGAGCACCGGCGTCCAGGCC 434
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de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
Wincker,P. and Weissenbach,J.
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T7 end of clone BB0AA001C03 of library BB0AA from strain CBS 4732
of Pichia angusta, genomic survey sequence.
                                                                                                                                                                                                                                              Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
                                                                                                                                                                                                                                                                                                                                              Pichia angusta
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
1 (bases 1 to 1021)
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/lab_host="E. coli DH10B"
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                     2102 GGACCAGCTCATTGCCGACGTGGCCGCCGCGAACCCCAAACACCGTCGTCGTCATGCAGAC 2161
                                                                                                                       2042 TAACGCCGACTGGGAGACCGAGGGCGCGACCGCGAGCATGAAGCTCCCCGGCGTGCT 210:
                                                                                                                                                                                                                            1982 AATCGAAAAGTCCGTCGCCCTCGCCAAGGAGCACGACCAGGTCATCATCTGCGCGGGCCT 2041
                                                                      303 CAATAAGGAATGGGAATCTGAAGGATCGGACAGGAAGAACATGAAACTTCCCGGCCATAA 362
                                                                                                                                                                        243 GATTCAGCAGGCAGCAGCAGCTCGCCAAGCTTCACAGGTTATTCTCGTTACAGGGCT 302
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/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BBOAA001C03"
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] [ Kluyveromyces marxianus ]"
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 Genoscope
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                                                                                                                                 Blandin, G., Llorente, B., Malpertuy, A., Wincker, P., Artiguenave, F
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Pichia angusta

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces Saccharomyces, kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
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/note="similar to P07337 [ Beta-glucosidase precursor BGLS ] [ Kluyveromyces marxianus ] "
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/db_xref="taxon:4905"
/clone="BBOAA015H01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="end :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="BBOAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.3%;
51.2%;
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Pred. No. 4.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 461; Indels
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ACCESSION DEFINITION RESULT 5 CNS075SU/c

970 bp

DNA

KEYWORDS VERSION

SOURCE

Kluyveromyces lactis. AL430516.1 GI:12213710

ORGANISM

REFERENCE

(bases

1 to 970)

AUTHORS

REFERENCE

(bases 1 to 970)

PUBMED

TITLE AUTHORS JOURNAL MEDLINE

REFERENCE

(bases 1 to 970)

Submission

AUTHORS

MEDLINE JOURNAL

Lett.

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66-70 (2000)

PUBMED

JOURNAL

COMMENT

lactis var.

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1557 GAGCCCCCTGGTACCCCTAACCGCCAGCACATTGACGAGCTCTTCTTCACCAAGACGGAC 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1674 GAGGGCACGTACACCGCCGACGAGGACTGCACCTACGAGCTCGGCCTCGTCGTCTGCGGC 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 CTTCCTGCTGAATCGTCTGACCGTGTCATTGTTGATGAGTTTGCATTGAATTCTACGAGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGCACCTGGTGGACTACTACCACCCCAAGGCGGCAGACA---CGTGGTACGCCGACATG 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGATGTTGTTTGATTACAAAAACGACAAACTAGACAACAACTTGTTCTATATGGATATC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGGCGAGTTTACCGCCAAAGAGACTGGCACCTACGAGATAAGCGTTAGTTGTCTTGGA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGATTTGCAGCCCTGGGTGCCTCTACCGCCCCAAAACCAAGAGATTTGATATGAACAAG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGATGCCTTCTTCGGCTCCGCCACCCGCGAGGAGACGGGCCGCATCAATCTCGTCAAG 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCGCACAATTTTTCATTAACGGTAAATTGGAGATTGATGACAAAAATAATCAAGTCCTT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kluyveromyces lactis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone BAOABO38CO8 of library BAOAB from strain CLIB 210 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekata,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kluyveromyces lactis, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic exploration of the hemiascomycetous yeasts: 1. yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
                                                                                                                                                                                      Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr | Web : www.genoscope:cns.fr | This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic exploration of the hemiascomycetous yeasts: Kluyveromyces_lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R., Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bolotin-Fukuhara, M., Toffano-Nioche, C., Artiguenave, F.,
                          angusta, Debaryomyces hansenii var. hansenii, Pichia sorbicopnii
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3
5 kb were prepared and both extremities were sequenced. See
                                                                                                                                  exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
keywords for description of this sequence and for the sequence of
                                                                                ar lactis, Kluyveromyces marxianus var marxianus, Pichia
Debaryomyces hansenii var hansenii, Pichia sorbitophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1002 ATCATGAGCGACTGGTACGGCACATACAGTACCACAGAAGCCGTTGTGGCAGGCCTCGAC 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        970 CAGGTAAATTGATGGGTAAGGAAGCCGTCGCCAAGAATGCTGCTGTGAT-TTTGGACCCA 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583 CAGGTAAGATGATGGGCAAAGAGGCCATCGCTAAGAGTGCGCATGTGATCCTCGGCCCGA 642
                                                 1344 GTCGGCCCCAACGCCAAGCAGGCCACATACCACGGCGGAGGCTCTGCCGCACTCAGGGCC 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1116 TCCAACGGAAAGCCCTTTATCCACGTCATTGACCAGAGGGCTAGGGAAGTTCTTCAGTTC 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1062 CTCGAGATGCCCGGACCTCCACGCTTCCGAGGAGAAACACTCAAGTTCAACGTC----- 1115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 643 CTATCAACATGCAACGCTCCCCTCTCGGTGGACGTGGCTTCGAGTCGATTGGTGAGGATC 702
                                                                                                                                                               1284 GTGCTGCTGAAGAACGAGAACAACGTTCTGCCCTTGAGCAAGAAGAAGAAGAAGACGCTGATT 1343
                                                                                                                                                                                                                                                                       1224 ACTGTCAACAACACCCCCGAAACGGCAGCTCTCCTCCGGAAGGTTGGCAACGAGGGCATC 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                762 CAGGCTACGATCAAGCACTTTTTGTGCAATGATCAGGAGGACAGGCGCATGATGGTGCAG 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    731 GCCACGCTCTCTGAGAGAGCGTTGCGAGAAATATACTTAGAACCTTTCAGATTGGCAGTC 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     822 AGCATCGTCACGGAGCGGGCTCTCCGTGAAATCTACGCACTCCCGTTCCAGATTGCTGTG 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 ATTGAGTTCCCAGGTCCAACGAGATGGAGAACTAATGAACTTGTTTCACATTCTCTAAAT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         551 ATTATGTCTGATTGGTTTGGTACTTACACCACTGCTGCTTCTATCAAGAATGGTCTGGAT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              611 TCTCAGAACAAAAATTGTTATTGGACATTCTTAGAAAAGAATGGAATTGGGATGGTATG 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  942 AGCGAGAACCCTAAATATCTTGATGGGATGCTTCGAAAGGAATGGGGTTGGGATGGCCTA 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         671 AAGAATGCTGATCCTGTTTGTTTAATGTCCGCTTACAATAAGGTGAACGGCGAACATTGT
                                                                                                                                                                                                                                                                                                                           371 ATTAAGTTTGTTCTTGACAACCAGGAAAAGACGGGGGATTGTTCAAAATGGTCCAGAAACC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTTCCTGGCGGGCTTGGGAGCTGCGGCTCTCATCCGCGGCATTCAGAGC-ACTGGAGTG 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAGACTCCCAGCCGGGTGCGTTCATGACGGCGTACAATGGCATCAATGGCGTGTCGTGC 941
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                                                                                                                                                                                                                                                                                                                                                                                  GTCAAGAAGTGTGCTGCCTCCGGAGTGACG------GAGAACGGCCCGAGACG 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCAGGGAACAAATTTCTATTTATGACGTTGACGACCGTGTTAGACAAGTTTTGAAAATG 372
                                                                                                           GTCTTGTTGAAGAACGAGAATTCGATTCTACCTTTGAAAAAAGAAGAATCAGTCGTCGTT 192
                                                                                                                                                                                                                      ACATCTAACAATAGTAAAGAGACCTCTGAATTGCTTAGAAAGATAGCTGCGGATTCCATT 252
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/note="similar to P07337 [ betaglucosidase
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221 c 174 g 284
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/clone="BA0AB038C08"
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Pred. No. 1.1e-15;
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                                        DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 20;
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                                                                                                                                                                                                                                                                                             AL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to keywords for description of this sequence and for the sequence of the other extremity of this insert.
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Kluyveromyces lactis
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                                                                                                                                                                                                                                                                                                                                             2133 AACCCAAACACCGTCGTCGTCATGCAGACGGGCACCCCCGAGGAGATGCCCTGGCTCGAC 2192
                                                                                                                                                                                                                                                                                                                                                                                                                                              2073 CGCGCGAGCATGAAGCTCCCCGGCGTGCTGGACCAGCTCATTGCCGACGTGGCCGCCGCG 2132
                                               2313 CTGCAGGACAACCCCGCGTTTCTCAACTTCCGCACCGAGGCCGGGGCGCACGCTGTACGGC 2372
                                                                                                                                             2253 GACGTCGTCTTGGCGACTACAACCCCTCGGGCAAGCTGTCCCTCAGCTTCCCCAAGCGC 2312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                880 AGGGAAGATATGACGTTGCCAGCAAGAACAAACGATCTAGTTCGTGCTGTATTGGAGGCT 821
                                                                                              700 GACGTCTTGTATGGTGATGTTGTYCCAAATGGGAAATTATCTCTCTCATGGCCATTAAAG
640 CTTGAAGACAATCCAGCTTATTTGAACTTCAAGACTGAATTTGGCAGAGTTGTCTACGGT 581
                                                                                                                                                                                                  AAAGCTAAKGCTCTGGTTCAAGCTTGGTACGGAGGCAATGAGCTGGGTAATGCTATTGCT 701
                                                                                                                                                                                                                                              GCCACGCCCGCCGTCATCCAGGCCTGGTACGGCGGCAACGAGACGGGCAACTCCATTGCC 2252
                                                                                                                                                                                                                                                                                                AACCCTAACACTGTAATTGTCAACCAGTCTGGTACTCCTGTCGAGTTCCCATGGTTACAA 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EWR Cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr ) Web: www.genoscope.cns.fr ) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F., Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R., Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M. Genomic exploration of the hemiascomycetous yeasts: 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) sequencing program of thirteen This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum; Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, saccharomyces kluyveri, Kluyveromyces thermotolejans, Kluyveromyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 TGAATTCGGAGCTGGTGCTCCAGGTTGGTGTTGCMAAGGCTATTGATGCAGATGAGGA 177
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/strain="CLIB 210"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Varrowia lipolytica. Genomic inserts of 3 to 8 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of
             426;
                               Similarity
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Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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FEBS Lett. 487 (1), 71-75 (2000)
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/note="similar to P07337 [ beta-glucosidase precursor (EC)
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/clone="AZ0AA011G05"
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                                                                                                                                                                                                                                                                                                                                                                                           TCAGCATCTATGAACTCCTACTATGTTGTTTCTCCGTATGAAGGTATCGTCAATAAGCTG 137
Souciet,J.L., Aiglė,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.
                                                                                  Eukaryota; Fungi; Ascomycota; Saccharo
Saccharomycetales; Saccharomycetaceae;
                                                                                                                    Kluyveromyces lactis
                                                                                                                                                                                                                   CNS072H1 745 bp DNA linear GSS clone BA0AB011D05 of library BA0AB from strain CLIB 210
                                                                                                                                                                     AL426203.1 GI:12209397
                                                                                                                                                                                                   Kluyveromyces lactis,
                                                                                                                                   Kluyveromyces lactis.
                                                                    (bases 1 to 745)
                                                                                                                                                                                                    genomic
                                                                                    Saccharomycotina; Saccl
cetaceae; Kluyveromyces
                                                                                                                                                                                                      survey sequence.
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                                                                                                     Saccharomycetes;
   Potier,S.
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Best Local
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CGCGAGGAGACGGCCCCATCAATCTCGTCAAGGGCCAACACGTACAAGTTCAAGATCGAG 1880
CCCTGGCTCGACGCCACGCCCGCCGTCATCCAGGCCTGGTACGGCGGCAACGAGACGGGC
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                                                                GTTTTGGAGGCCAATCCTAACACTGTAATTGTYAACCAGTCTGGTACTCCTGTCGAGTTC
                                                                                                                                 GTGGCCGCCGCGAACCCCAAACACCGTCGTCGTCATGCAGACGGGCACCCCCGAGGAGATG
                                                                                                                                                                                              GAAGGTCATGATAGGGAAGATATGACTTTGCCAGGAAGAACAAACGATCTCGTCCGTGCT
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yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saurin, W., \ \ Tekaia, F., \ \ Toffano-Nioche, C., \ \ Wesolowski-Louvel, M., \\ Wincker, P. \ \ and \ \ Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 kb were prepared and both extremities were sequenced keywords for description of this sequence and for the sethe other extremity of this insert.
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/strain="CLIB 210"
/variety="lactis"
/db_xref="taxon:28985"
/clone="BaOABO11D05"
/clone_1lb="BAOABB"
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           5 kb were prepared and both extremities were sequenced. See-
keywords for description of this sequence and for the sequen
the other extremity of this insert.
Location/Qualifiers
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Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
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Saccharomycetales; Saccharomycetaceae; Pichia.
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                                                                                                                                                                                                                                                                                                                                                     76-81 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                            Artiguenave, F.
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1642 CCAAGGCGGCAGACACGTGGTACGCC---GACATGGAGGGCACGTACACCGCCGACGACGAGG 1698
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ACAAACTAGACAACATTGTTCTATATGGATATCGAGGGCGAGTTTACCGCCAAAGAGA 849
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/evidence=not_experimental
193 c 231 g 289 t
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/note="similar to P07337 [ Beta-glucosidase precursor BGLS
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/strain="CBS 4732"
/db_xref="taxon:4905"
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Pred. No. 3e-12,
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T3 end of clone BB0AA003F03 of library BB0AA from strain CBS 4732
of Pichia angusta, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EWRY cedex, FRANCE. (E-mail: segref@genoscope.cns.fr ) Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic exploration of the hemiascomycetous yeasts: 13. Pichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blandin, G., Llorente, B., Malpertuy, A., Wincker, P., Artiguenave, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                         angusta, Debaryomyces hansenil var. Hansenil, Figure 2012 of 3 to Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exiguus, Saccharomyces servazzii, zygosaccharomyces rouxii, saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lactis var.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ar lactis, Kluyveromyces marxianus var marxianus,
Debaryomyces hansenii var hansenii, Pichia sorbi
                                                                               /evidence=not_experimental
237 c 195 g 274
                                                                                                                                                                           complement(<27.
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/clone="BB0AA003F03"
                                                                                                                                                                                                                                                                                           organism="Pichia angusta"/strain="CBS 4732"
                                                                                                                       /note="similar to p07337 [ Beta-glucosidase precursor BGLS ] [ Kluyveromyces marxianus ]"
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
          5.3%;
                                                                                                                                                                                                                              lib="BBOAA"
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            Score 158.4;
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               DB 17;
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                                                                                    1 others
            Length 986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1515 ACGCCCGACGGCGCTCCGGGCATGCGCTGGAGGGTCTTCAACGAGCCCCCTGGTACCCCT 1574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1575 AACCGCCAGCACATTGACGAGCTCTTCTTCACCAAGACGGACATGCACCTGGTGGACTAC 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1635 TACCACCCCAAGGCGGCAGACA---CGTGGTACGCCCGACATGGAGGGCACGTACACCGCC 1691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1752 GACGACCAGCTCGTCGACAACGCCACCAAGCAGGTCCCCGGGGATGCCTTCTTCGGC 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1986 GAAAAGTCCGTCGCCCTCGCCAAGGAGCACGACCAGGTCATCATCTGCGCGGGCCTTAAC 2045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1928 -- CGGCCACGGCTCCCCTCCGCGTCGGCGGCTGCAAGGTCATTGACGACCAGGCCGAAATC 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1812 TCCGCCACCCGCGAGGAGACGGGCCGCATCAATCTCGTCAAGGGCAACACGTACAAGTTC 1871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          827 ACCTTCAACGGTTCCGAAGGGGTTTATTGCAAGGTTTACAACCTTCCTGCTGAATCGTCT 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1872 AAGATCGAGTTCGGCTCCGCACCCACCTACACCCTCAAGGGCGACACCATCGTCCC---- 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               647 AAAGAGACTGGCACCTACGAGATAAGCGTTAGTTGTCTTGGAACCGCCACATTTTTCATT 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      767 GACCGTGTCATTGTTGATGAGTTTGCATTGAATTCTACGAGATTGATGTTGTTTGATTAC 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2166 ACCCCCGAGGAGATGCCCTGGCTCGACGCCACGCCCGCCGTCATCCAGGCCTGGTACGGC 2225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2106 CAGCTCATTGCCGACGTGGCCGCCGCAACCCCAAACACCGTCGTCGTCATGCAGACGGGC 2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2046 GCCGACTGGGAGACCGAGGGCGCGACCGCGGGGAGCATGAAGCTCCCCGGCGTGCTGGAC 2105
                                                                                                                                                                                                                                                                                                                                                                                                                                                2226 GGCAACGAGACGGGCAACTCCATTGCCGACGTCGTCTTTGGCGACTACAACCCCTCGGGC 2285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467 AAGATTGAGTTTGGTTCGGGTCCAACGTTCACTTTGGAGACCACTGATCTAGTTGCATCT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          527 GCCTCTACCGCCCCAAAACCAAGAGATTTGATATGAACAAGGGAGAGTCTTTCAAATAC 468
                                                                                                                                                                                                                                                                                                                                                              2286 AAGCTGTCCCTCAGCTTCCCCAAGCG 2311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 TCAGATTGGGAGAGTGAGGGATACGATAGACCAGTTATGGACCTTCCTGGTAGCCAGGAT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 AAAAAGGCTGTTGAAGTTGCATCACAAACTGATAAAGTTGTTCTCTGTGTTGGAACATCA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 ACCCCAGTCACGATGCCATGGGTCGATGAGGTTCCGGCTATAATTCAGGGATGGTTCAAT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 GAGCTCATCCAAGAAGTCCTTAAAGTCAACAAGAATGTGGTGGTAGTCAAT¢TTTCCGGT 168
                                                                                                                                                                                                                                                                                                                                                                                                       47 AAATTGAGTTTAACATTCCCTAAACG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACGGTAAATTGGAGATTGATGACAAAAATAATCAAGTCCTTGGATTTGCAGCCCTGGGT 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACGGAGGAGGAGCGCTCTATGTTTCCGCCATGAAGGTCGGAGTCGGATAAGGATAGGATC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416;
                                          Kluyveromyces lactis
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                         CNS074WR 836 bp DNA linear GSS 07-JUL-2001 clone BA0AB031C06 of library BA0AB from strain CLIB 210 of
                      Saccharomycetales; Saccharomycetaceae; Kluyveromyces
                                                                                                                                                     AL429361
                                                                                        Kluyveromyces lactis.
                                                                                                                              AL429361.1 GI;12212555
                                                                                                                                                                       Kluyveromyces lactis, genomic survey sequence
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(bases 1 to 836)
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                                                      1838 CATCAATCTCGTCAAGGGCAACACGTACAAGTTCAAGATCGAGTTCGGCTCCGCACCCAC 1897
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                                                                                                                                                                                                                                                                                 1778 CACCAAGCAGGTCCCCGGCGATGCCTTCTTCGGCTCCGCCACCCGCGAGGAGACGGGCCG 1837
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342 AAGTGAGTTGGTGAGTGA------ATTTGGATCTGGCGGTTTTCAAGTTGGTGTTGC 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                               282 TGTCAGTCTGCAAAAGGGTAAAGCGTATAAMGTTAGAATCGAATACGGTTCTGGTCCAAC
                                                                                                                                                                                                                           222 GAMAGACCAAACTCGTGGAAGTTTCTGCTTCGGTGCTGCTACCGATGAAAAGACCAAGAC 281
                                                                                                                                                                                                                                                                                                                                          162 TTTACTGGTTTACGGCACCGGCATATTGTACTTGGATGAATTAGTGGTTGATCAGAA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 GTTCTACATCACACTGGAAGGTTACTTTACTCCTAAAGAAGATGCCAACTACCTTTTCGG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Showere prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                CCTCGTCGTCTGCGGCACGGCAAAGGCGTACGTAGACGACCAGCTCGTCGTCGACAACGC 1777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kluyveromyces lactis
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163 c 192 g 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to P07337 [ betaglucosidase ]"
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<7. .>780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:28985"
/clone="BA0AB031C06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /variety="lactis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Kluyveromyces lactis"
/strain="CLIB 210"
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
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                                                                                                                                                                                                                                                                                                                                         Blandin, G., Llorente, B., Malpertuy, A., Wincker, P., Artiguenave, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Liorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                              angusta
                                                                                                                                                                                                                                                                                                   Genomic
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AL432099
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                                                         2262 TITGGCGACTACAACCCCTCGGGCAAGCTGTCCCTCAGCTTCCCCAAGCGCCTGCAGGAC 2321
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362 GTCATACTTTGTATTGGAACCTCCAACGAATTGGAGAGCGAGGGATTTGACCGGCCTCAC 303
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                                                                                                                                182 GCACTTTTACACGGATGGTTTAATGGGAATGGAATCAGGAAATGCTATTGCAGACGTACTA 123
                                                                                                                                                                                                                                                              242 GTGATTCTAGTCAATCTATCTGGCACGCCTGTAACTCTCCCTTGGATAGATGACGTCCCT 183
                                                                                                                                                                                                                                                                                                                                                                                           ATGGATCTTCCAAAACTTCAAAATAAGCTTGTTGACGAAATACTGAAAGTCAACAGGAAC 243
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/note="similar to P07337 [ Beta-glucosidase precursor BGLS] [ Rluyveromyces marxianus ]"
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0; Mismatches 358
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                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F., Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R., Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M. Genomic exploration of the hemiascomycetous yeasts: 11. Kluyveromyces lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
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Kluyveromyces lactis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                         5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                           lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowla lipolytica. Genomic inserts of 3 to
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/clone="BA0AB036G05"
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                                      2749 TTATCGTGAGC 2759
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583 TCTTGGTAGGC 593
                                                                        523 CTATTTCCTTCGATGAAGAAGTCGGTAAGTGGTGTTCAGAAGCTGGTCAGTACAAAG 582
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